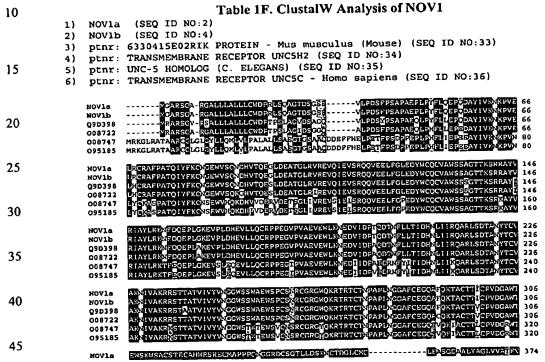
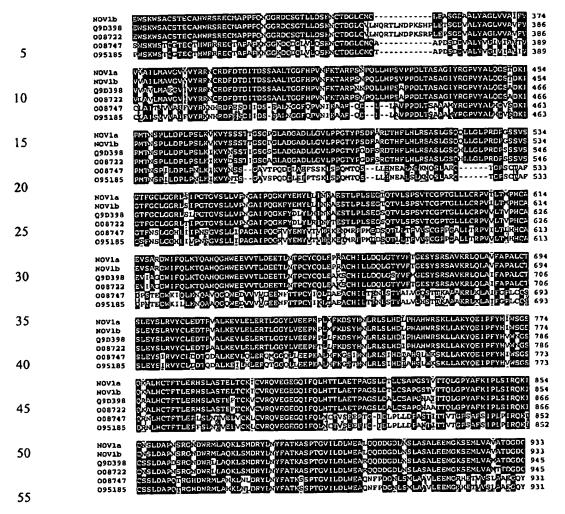
Table 1E. BLAST results for NOV1a						
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect	
ptnr:SPTREMBL- ACC:Q9D398	6330415E02RIK PROTEIN - Mus musculus (Mouse)	945	862/945 (91%)	897/945 (94%)	0.0	
ptnr:SPTREMBL- ACC:008722	TRANSMEMBRANE RECEPTOR UNCSH2	945	862/945 (91%)	893/945 (94%)	0.0	
ptnr:SPTREMBL- ACC:008747	UNC-5 HOMOLOG (C. ELEGANS)	931	610/929 (65%)	723/929 (77%)	0.0	
ptnr:SPTREMBL- ACC:095185	TRANSMEMBRANE RECEPTOR UNC5C - Homo sapiens	931	598/929 (64%)	718/929 (77%)	0.0	

The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 1F. In the ClustalW alignment of the NOV1 proteins, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be altered to a much broader extent without altering protein structure or function.





The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (http:www.ebi.ac.uk/ interpro). DOMAIN results for NOV1 as disclosed in Tables 1G-1O, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. For Tables 1G-1O and all successive DOMAIN sequence alignments, fully conserved single residues are indicated by black shading or by the sign (|) and "strong" semi-conserved residues are indicated by grey shading or by the sign (+). The "strong" group of conserved amino acid residues may be any one of the following groups of amino acids: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW.

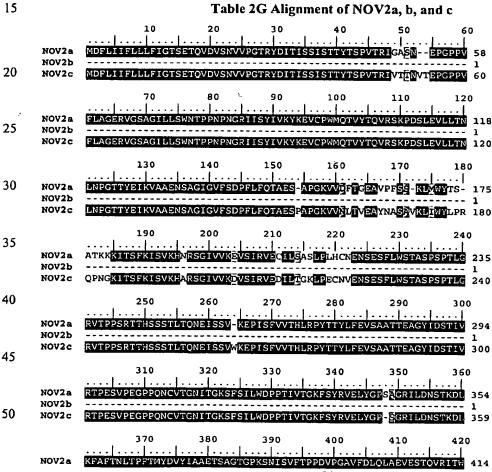
Precursor (EC 3.1.3.48)) (E = 0.0). Public amino acid databases include the GenBank databases, SwissProt, PDB and PIR.

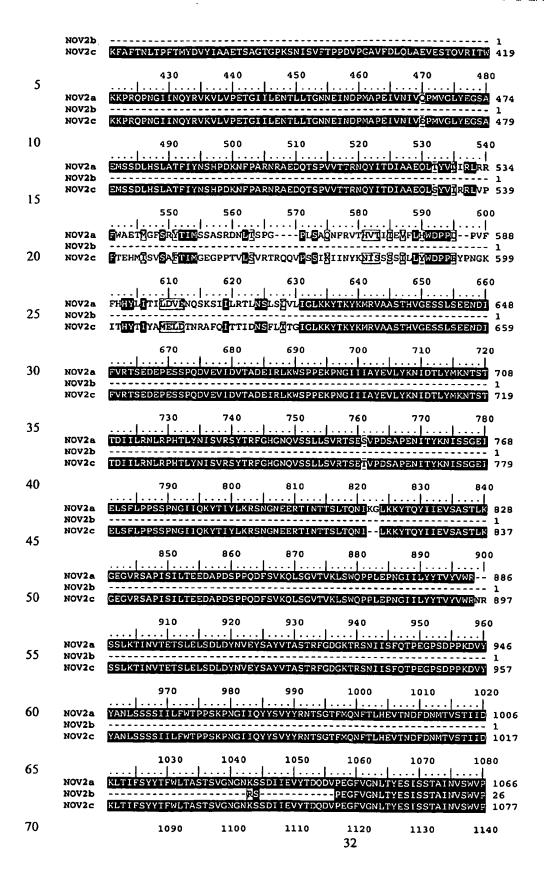
5

10

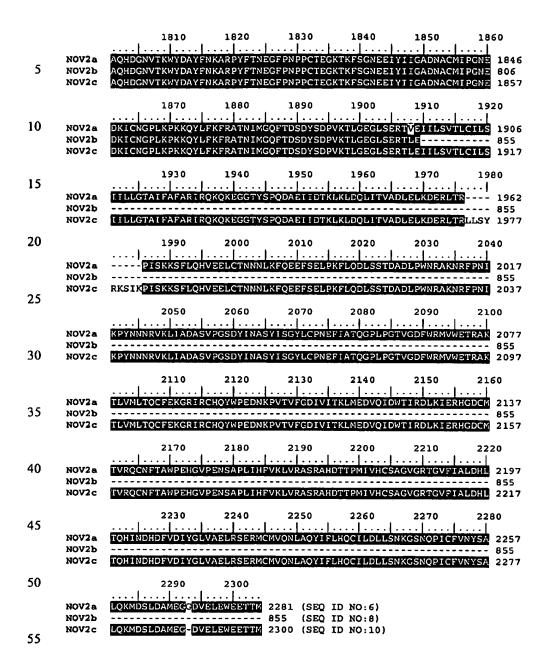
NOV2c is expressed in at least Synovium/Synovial membrane, Kidney. Expression information was derived from the tissue sources of the sequences that were included in the derivation of the sequence of CuraGen Acc. No. CG50718-05. The sequence is predicted to be expressed in the *Rattus norvegicus*: glomerular mesangial. because of the expression pattern of (GENBANK-ID: gb:GENBANK-ID:AF063249|acc:AF063249.1) a closely related *Rattus norvegicus* glomerular mesangial cell receptor protein-tyrosine phosphatase precursor (PTPRQ) mRNA, complete cds homolog.

Homologies among each of the above NOV2 proteins will be shared by the other NOV2 proteins insofar as they are homologous to each other as shown below in Table 2G. Any reference to NOV2 is assumed to refer to all three of the NOV2 proteins in general, unless otherwise noted.

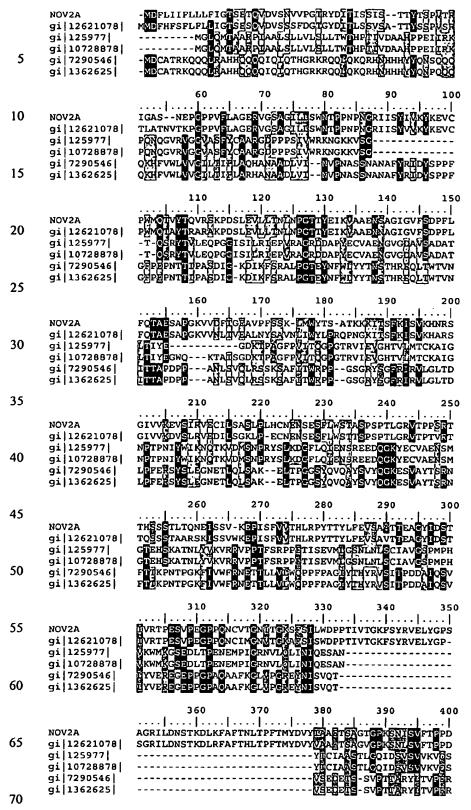


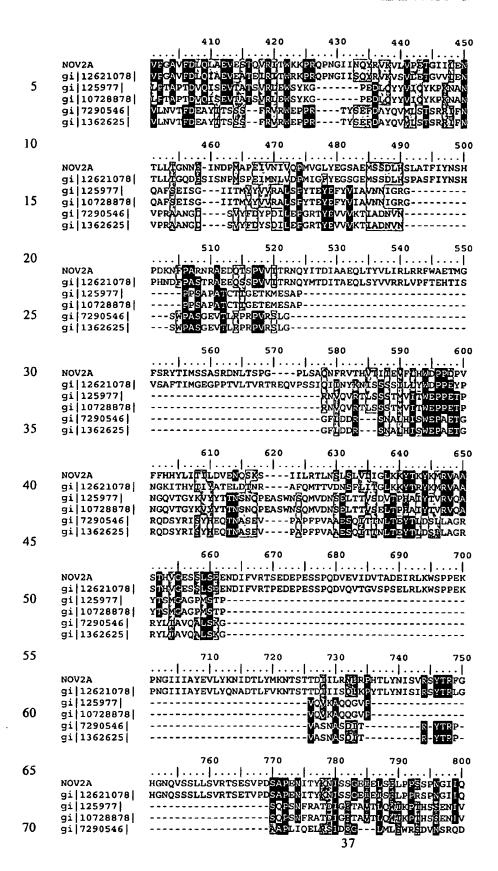


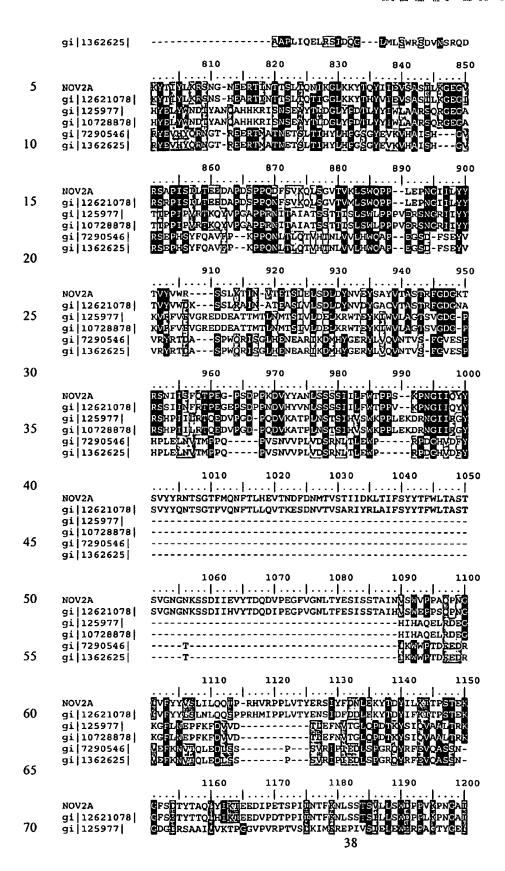
5	NOV2a NOV2b NOV2c	PAQPNGLVFYYVS PAQPNGLVFYYVS	SLILQQTPRHVRPE SLILQQTPRHVRPE SLILQQTPRHVRPE 1160	PLVTYERSIYE PLVTYERSIYE	DNLEKYTDY I	LKITPSTEKO LKITPSTEKO LKITPSTEKO	FSDT 1126 FSDT 86 FSDT 1137
10	NOV2a NOV2b NOV2c	YTAQLYIKTEEDI YTAQLYIKTEEDI YTAQLYIKTEEDI	PETSPIINTFKNI PETSPIINTFKNI PETSPIINTFKNI	LSSTSVLLSWE LSSTSVLLSWE	DPPVKPNGAII DPPVKPNGAII DPPVKPNGAII	SYDLTLQGPN SYDLTLQGPN SYDLTLQGPN	ENYS 1186 ENYS 146 ENYS 1197
15	NOV2a NOV2b NOV2c	FITSDNYIILEEL FITSDNYIILEEL FITSDNYIILEEL	1220 .   . .SPFTLYSFFAAAR .SPFTLYSFFAAAR .SPFTLYSFFAAAR	RTRKGLGPSSI RTRKGLGPSSI RTRKGLGPSSI	LFFYTDESVP LFFYTDESVP LFFYTDESVP	LAPPONLTLI LAPPONLTLI LAPPONLTLI	NCTS 1246 NCTS 206 NCTS 1257
20	NOV2a NOV2b NOV2c	DFVWLKWSPSPLE	GGIVKVYSFKIHE	HETOTIYYKN	ISGFKTEAKL ISGFKTEAKL	VGLEPVSTYS VGLEPVSTYS	IRVS 1306 IRVS 266
25	NOV2a NOV2b NOV2c	AFTKVGNGNQFSN	1340 .       . IVVKFTTQESVPDV IVVKFTTQESVPDV	/VQNMQCMATS /VQNMQCMATS	WQSVLVKWDP WQSVLVKWDP	PKKANGIITQ PKKANGIITQ	YMVT 1366 YMVT 326
30		1390	1400 .   .	1410	1420	1430	1440
35	NOV2a NOV2b NOV2c	VERNSTKVSPQDH	MYTFIKLLANTSY MYTFIKLLANTSY	VFKVRASTSA VFKVRASTSA	GEGDESTCHV GEGDESTCHV	STLPETVPSV STLPETVPSV	PTNI 1426 PTNI 386
	NOV2a	AFSDVQSTSATLT	.   . WIRPDTILGYFQN	YKITTQLRAC	KCKEWESEEC	VEYOKIOYLY	 PAH 1486
40	NOV2b NOV2c	AFSDVQSTSATLT AFSDVQSTSATLT	WIRPDTILGYFQN	IYKITTQLRAQ	KCKEWESEEC	VEYQKIQYLY	EAHL 446
		1510	1520 .   .	1530	1540	1550	1560
45	NOV2a NOV2b NOV2c	TEETVYGLKKFRW TEETVYGLKKFRW TEETVYGLKKFRW	YRFQVAASTNAGY YRFQVAASTNAGY	'GNASNWISTK 'GNASNWISTK	TLPGPPDGPP TLPGPPDGPP	ENVHVVATSP ENVHVVATSP	FSIS 1546 FSIS 506
50		1570	1580 .  .	1590   .	1600   .	1610   -	
30	NOV2a NOV2b NOV2c	ISWSEPAVITGPT ISWSEPAVITGPT ISWSEPAVITGPT	CYLIDVKSVDNDE	FNISFIKSNE	ENKTIEIKDL	EIFTRYSVVI	TAFT 566
55		1630 	1640 .	1650   .	1660   .	1670   .	1680 ···
	NOV2a NOV2b NOV2c	GNISAAYVEGKSS GNISAAYVEGKSS GNISAAYVEGKSS	AEMIVTTLESAPK	DPPNNMTFQK	I PDEVTKFQL'	TSLPPSOFNG	NIOV 626
60		1690	1700 .   .	1710	1720	1730	1740 
65	NOV2a NOV2b NOV2c	YQALVYREDDPTA YQALVYREDDPTA YQALVYREDDPTA	VQIHNLSIIQKTN VQIHNLSIIQKTN	TFVIAMLEGL TFVIAMLEGL	KGGHTYNISV KGGHTYNISV	YAVNSAGAGP YAVNSAGAGP	KVPM 1726 KVPM 686
0.5		1750	1760 .  .	1770	1780	1790	1800
70	NOV2a NOV2b NOV2c	RITMDIKAPARPK RITMDIKAPARPK RITMDIKAPARPK	TKPTPI YDATGKL TKPTPI YDATGKL	LVTSTTITIR LVTSTTITIR	MPICYYSDDHO MPICYYSDDHO	GPIKNVOVLV	1786 1906 746

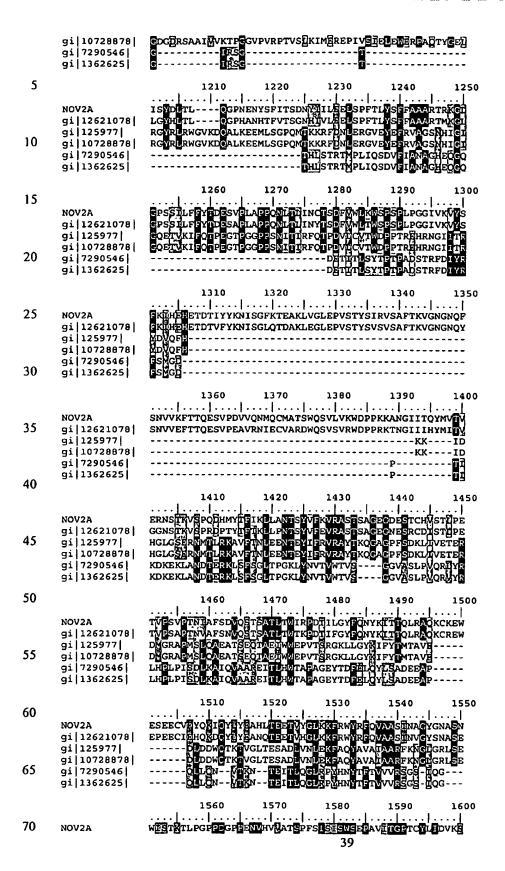


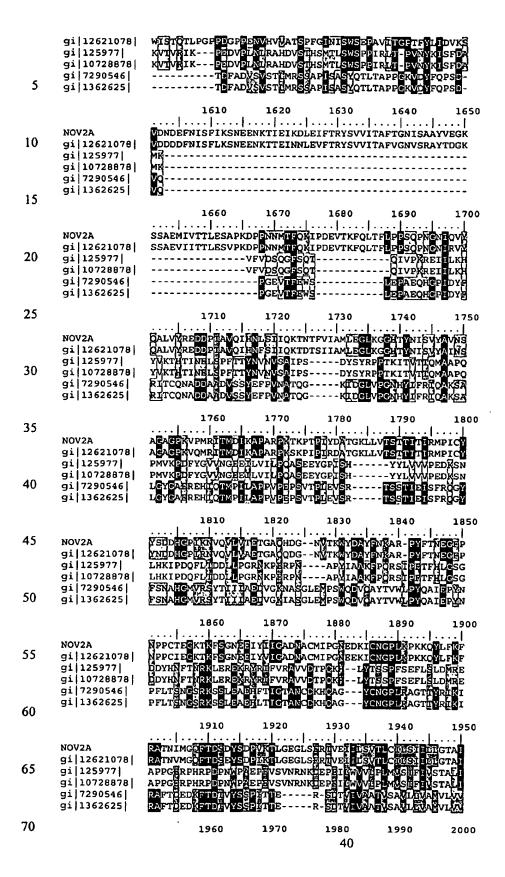
The disclosed NOV2a polypeptide has homology to the amino acid sequences shown in the BLASTP data listed in Table 2H.











5	NOV2A gi 12621078  gi 125977  gi 10728878  gi 7290546  gi 1362625	FAPARIROKOKEGGTYSPODABINDTKLKLDOLITVAD ETKOER FAPARIROKOKEGGTYSPODABINDTKLKLDOLITVAD ETKOER FAFVRIROKO
10	NOV2A gi 12621078  gi 125977  gi 10728878  gi 7290546  gi 1362625	2010 2020 2030 2040 2050
20 25	NOV2A gi 12621078  gi 125977  gi 10728878  gi 7290546  gi 1362625	2060 2070 2080 2090 2100  TTADLEWNRAKNREPNIK PYNNNRVKLIADAS VEGSDYINAS YNSGYLCF DADLEWNRAKNREPNIK PYNNNRVKLIADVS VEGSDYINAS YVSGYLCP DASNLEHNKSKNRVANVTAYDHSRVOLPAVEGVYGSDYINANYCDGYRKH DISNLEHNKSKNRVANVTAYDHSRVOLPAVEGVYGSDYINANYCDGYRKH SFANLEDNRPKNRFTNIL PYDHSREKLOPVDDDDGSDYINANY PEHNSP SFANLECNRPKNRFTNIL PYDHSREKLOPVDDDDGSDYINANY PEHNSP
30 35	NOV2A gi 12621078  gi 125977  gi 10728878  gi 7290546  gi 1362625	2110 2120 2130 2140 2150  NEFIATOGPLPGTVGDFWRMWEITRAKTIVMLTCFEKGRIRGHOYWPED NEFIATOGPLPGTVGDFWRMWEITRKTLVMLTCFEKGRIRGHOYWPED NAYVATOGPLOETFVDFWRMCWEILHTATIVMTRLEERTRIKCDQYWPTR NAYVATOGPLOETFVDFWRMCWEILHTATIVMTRLEERTRIKCDQYWPTR REFIVTOGPLHSTREEFWRMCWEINSRAIVMLTRCFEKGREKCDOYWPVD REFIVTOGPFHSTREEFWRMCWEINSRAIVMLTRCFEKGREKCDOYWPVD
40	NOV2A gi 12621078  gi 125977  gi 10728878  gi 7290546  gi 1362625	2160 2170 2180 2190 2200
45 50	NOV2A gi 12621078  gi 125977  gi 10728878  gi 7290546  gi 1362625	2210 2220 2230 2240 2250  EHGVPENSAPLÜHFVÄLVRASRAHDÜTPMIVHCSAGVGRTGVFIALDHÜT EHGVPENTTPLEHFVÄLVRTSRAHDÜTPMVVHCSAGVGRTGVFIALDHÜT DHGVPENPAFFÄÖFLRRCRAFTPPESGPVIVHCSAGVGRTGCYIVÜDSML DHGVPENPAFFÄÖFLRRCRAFTPPESGPVIVHCSAGVGRTGCYIVÜDSML DFGVPEPPOSEVRFVRAFROMIGTOMRPIIVHCSAGVGRSGTFIALDRÜL DFGVPEPPLSEVRFVRAFROMIGTOMRPIIVHCSAGVGRSGTFIALDRÜL
55 60	NOV2A gi 12621078  gi 125977  gi 10728878  gi 7290546  gi 1362625	2260 2270 2280 2290 2300
65 70	NOV2A gi 12621078  gi 125977  gi 10728878  gi 7290546  gi 1362625	2310 2320 2330 2340 2350
		41

	NOV2A	2360 2370 2380 2390 2400
5	gi 12621078  gi 125977  gi 10728878  gi 7290546	NLPCNKHRABLVHILPYESSRVYLTPIHGIEGSDYVNASFIDGYRYRSRY NLPCNKHRABLVHILPYESSRVYLTPIHGIEGSDYVNASFIDGYRYRSRY DEDEDGEOGOOOOO
10	gi 1362625	DEDED G G G G G G G G G G G G G G G G G
15	NOV2A gi 12621078  gi 125977  gi 10728878  gi 7290546  gi 1362625	IAAGGPVORAAEDFWRMLWEHVSTIVVMLTKLKEMGREKCFQYWPHERSV IAACGPVORAAEDFWRMLWEHVSTIVVMLTKLKEMGREKCFQYWPHERSV DDEEDBEDDDDDDDDDQQPLNNETTATYSSASCSSSTHDVHV DDEEDBEDDDDDDDDQQPLNNETTATYSSASCSSSTHDVHV
20		2460 2470 2480 2490 2500
25	NOV2A gi 12621078  gi 125977  gi 10728878  gi 7290546  gi 1362625	RYCYYMVDEIAEYNMPQYKLREFKVTDARDGSSRTVRÖFQFIDWPECCVP RYCYYMVDFIAEYNMPQYKLREFKVTDARDGSSRTVRÖFQFIDWPECCVP VLOEADEKEKQEQERICAGTGSHADTESDNTDSDDDDEDGDGKVAKDCAV VLOEADEKEKQEQERICAGTGSHADTESDNTDSDDDDEDGDGKVAKDCAV VLOEADEKEKQEQERICAGTGSHADTESDNTDSDDDDEDGDGKVAKDCAV
30	NOV2A gi 12621078	2510 2520 2530 2540 2550
35	gi 125977  gi 10728878  gi 7290546  gi 1362625	KSGEGIDFIGQVHKTKEQFGQDGPITVHCSAGVGRSGVFITLSIVLERM KSGEGIDFIGQVHKTKEQFGQDGPITVHCSAGVGRSGVFITLSIVLERM ADEDGWYYADEDGWYYADEDGWYY
40	NOV2A gi 12621078  gi 125977	2560 2570 2580 2590
45	gi 10728878  gi 7290546  gi 1362625	QYEGVLDVFQTVRILRSQRPAMVQTEDQYHFCYRAALEYLGSFDNYTN

Tables 2J-2EE list the domain descriptions from DOMAIN analysis results against NOV2a. This indicates that the NOV2a sequence has properties similar to those of other proteins known to contain this domain.

```
Table 2J. Domain Analysis of NOV2a

gnl|Smart|smart00194, PTPc, Protein tyrosine phosphatase, catalytic domain (SEQ ID NO:93)

CD-Length = 264 residues, 99.6% aligned

Score = 318 bits (816), Expect = 2e-87
```

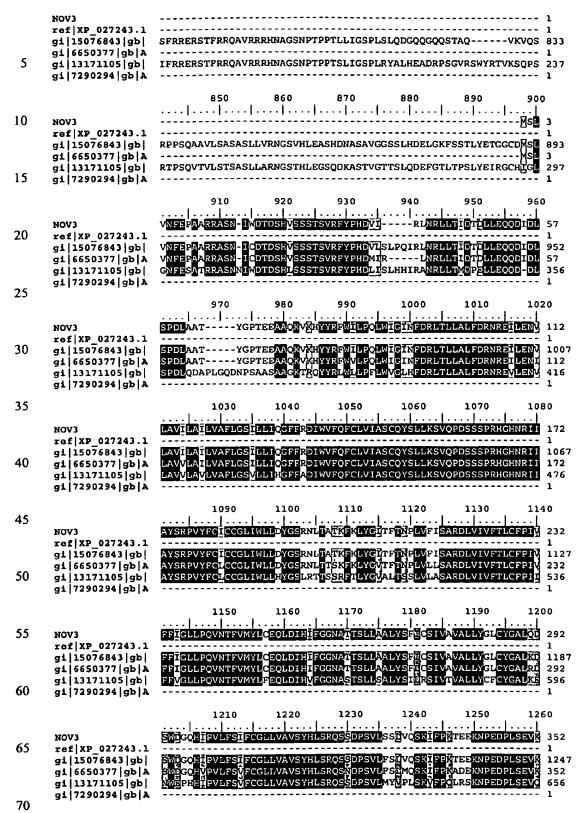
The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 3D.

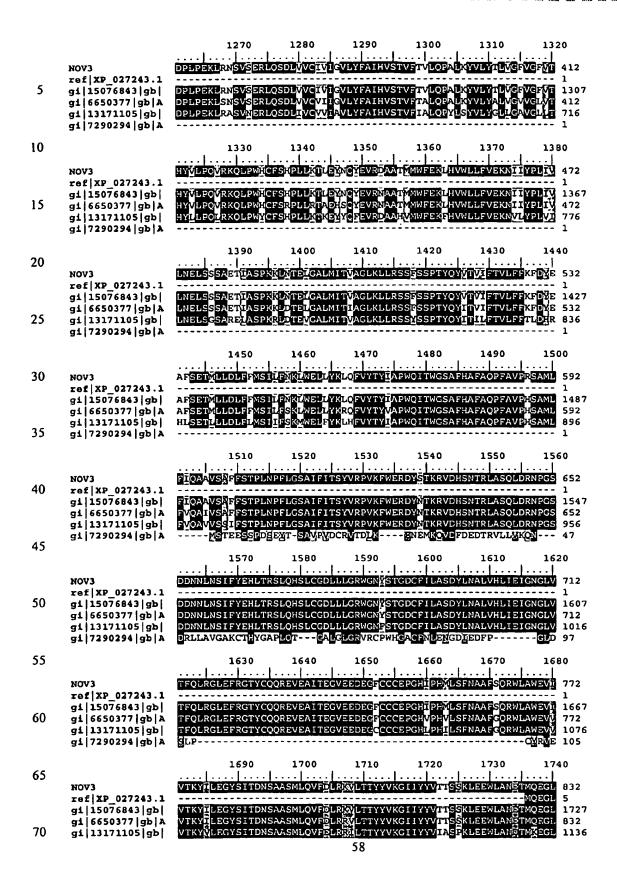
# Table 3D. ClustalW Analysis of NOV3

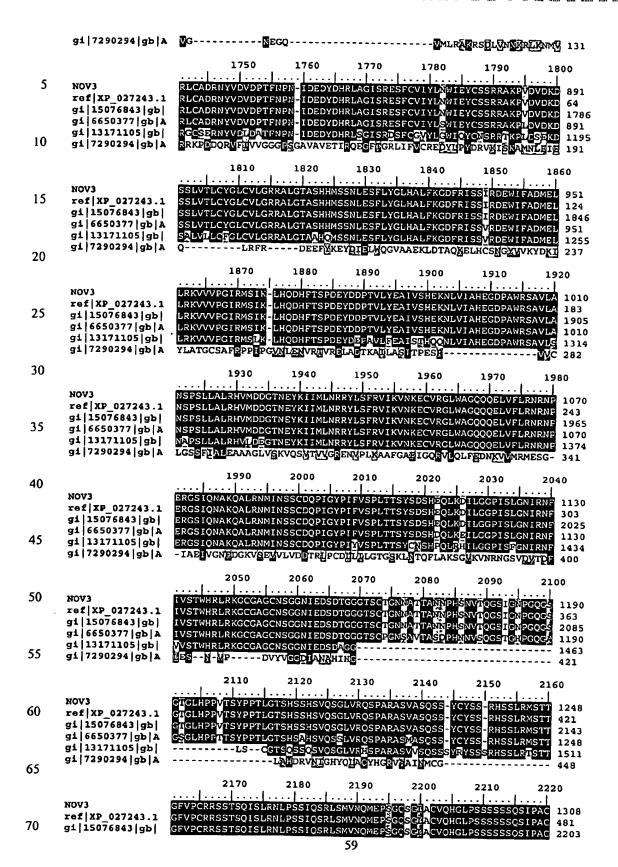
		č
5	1) NOV3 (SEQ ID	
		3.1 (XM_027243) hypothetical protein XP_027243 (Homo sapiens) (SEQ
	ID NO:42)	gb AAK82958.1 AF233450_1 (AF233450) pecanex-like protein 1 (Homo
	3) gi 15076843  sapiens) (SEQ ID	
10		b AAF21809.1 AF096286_1 (AF096286) pecanex 1 (Mus musculus) (SEQ ID
	NO:44)	·
	5) gi 13171105	gb AAK13590.1 AF154413_1 (AF154413) pecanex (Takifugu rubripes) (SEQ
	ID NO:45)	
1.5		b AAF45755.1  (AE003423) pcx gene product [alt 1] [Drosophila
15	melanogaster) (S	EQ ID NO:46)
		10 20 30 40 50 60
20	NOV3	1
	ref XP_027243.1	1
	gi 15076843 gb  gi 6650377 gb A	MGSQTLQILRQGVWAALSGGWYYDPHQATFVNALHLYLWLFLLGLPFTLYMALPSTMIIV 60
	gi 13171105 gb	MGSQTLQILRQGVWASVTGGWYYDPDQNTFVNALHLYIWLFLLCFPFTLYMALQPSMVIV 60
25	gi  7290294  gb   A	1
		70 80 90 100 110 120
	NOV3	
30	ref XP 027243.1	
	gi   15076843   gb	AVYCPVIAAVFIVLKMVNYRLHRALDAGEVVDRTANEFTDQR-TKAEQGNCSTRRKDSNG 119
	gi   6650377   gb   A	······ 1
	gi 13171105 gb  gi 7290294 gb A	GIYCGVIAAMFLLLKTVNYRLHHALDEGEVVEHQTRESKGSRGGTGGANDPVTRREDSNG 120
35	g1 /290294 gb X	1
		130 140 150 160 170 180
	NOV3	1
40	ref XP_027243.1 gi 15076843 gb	PSDPGGGIEMSEFIREATPPVGCSSRNSYAGLDPSNQIGSGSSRLGTAATIKGDTDTAKT 179
	gi 6650377 gb A	1
	gi   13171105   gb	LGDPGGGIEMADFIRQETPPVDCSSRNSYVG 151
	gi 7290294 gb A	
45		190 200 210 220 230 240
73		190 200 210 220 230 240
	NOV3	····[····]····]····]····]····]···]···]·
	ref   XP_027243.1	
50	gi 15076843 gb	SDDISLSLGQSSSLCKEGSEEQDLAADRKLFRLVSNDSFISIQPSLSSCGQDLPRDFSDK 239
30	gi 6650377 gb A gi 13171105 gb	151
	gi 7290294 gb A	151
	• , , , ,	
c c		250 260 270 280 290 300
55	170113	
	NOV3 ref XP 027243.1	1
	gi 15076843 gb	VNLPSHNHHHHVDQSLSSACDTEVASLVPLHSHSYRKDHRPRGVPRTSSSAVAFPDTSLN 299
	gi   6650377   gb   A	
60	gi 13171105 gb	151
	gi 7290294 gb A	1
		310 320 330 340 350 360
65	NOV3	1
	ref   XP_027243.1	1
		6.6

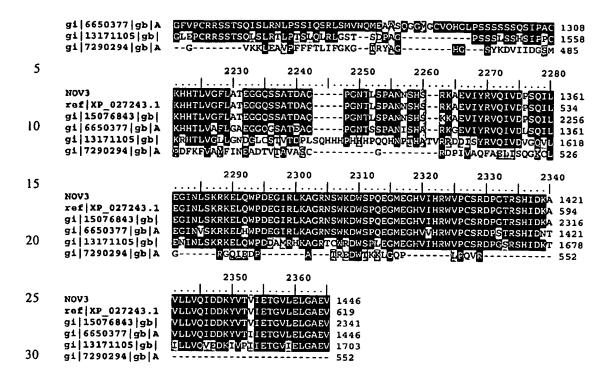
	gi 15076843 gb  gi 6650377 gb A gi 13171105 gb  gi 7290294 gb A	DFPLYQQRRGLDPVSELESSKPLSGSKESLVENSGLSGEFQLAGDLKINTSQPPTKSGKS 359
5	31   14 30 5 3 4 1 3 D   Y	-
	NOV3	370 380 390 400 410 420 
10	ref XF_027243.1 g1 15076843 gb  g1 6650377 gb A g1 13171105 gb	KPLKAEKSMDSLRSLSTRSSGSTESYCSGTDRDTNSTVSSYKSEQTSSTHIESILSEHEE 419
15	gi 7290294 gb A	430 440 450 460 470 480
13	*****	
20	NOV3 ref[XP_027243.1 gi 15076843 gb  gi 6650377 gb A gi 13171105 gb  gi 7290294 gb A	1 SPKAGTKSGRKKECCAGPEEKNSCASDKRTSSEKIAMEASTNSGVHEAKDPTPSDEMHNQ 479
25	NOV3	490 500 510 520 530 540 
30	ref XP_027243.1 gi 15076843 gb  gi 6650377 gb A gi 13171105 gb  gi 7290294 gb A	1 RGLSTSASEEANKNPHANEFTSQGDRPPGNTAENKEEKSDKSAVSVDSKVRKDVGGKQKE 539
35	NOV3	550 560 570 580 590 600 
	ref XP_027243.1 g1 15076843 gb  g1 6650377 gb A g1 13171105 gb	1   GDVRPKSSSVIHRTASAHKSGRRRTGKKRASSFDSSRHRDYVCFRGVSGTKPHSAIFCHD   599   1   173
40	gi 7290294 gb A	610 620 630 640 650 660
45	NOV3 ref[XP_027243.1 gi 15076843 gb  gi 6650377 gb A	EDSSDQSDLSRASSVQSAHQFSSDSSSTTSHSCQSPEGRYSALKTKHTHKERGTDSEHT 659
50	gi 13171105 gb  gi 7290294 gb A	
	иоvз	670 680 690 700 710 720 
55	ref xP_027243.1 gi 15076843 gb  gi 6650377 gb A gi 13171105 gb  gi 7290294 gb A	HKAHLVPEGTSKKRATRRTSSTNSAKTRARVLSLDSGTVACLNDSNRLMAPESIKPLTTS
60	NOV3	730 740 750 760 770 780 
65	ref XP_027243.1 gi 15076843 gb  gi 6650377 gb A gi 13171105 gb  gi 7290294 gb A	KSDLEAKEGEVLDELSLLGRASQLETVTRSRNSLPNQVAFPEGEEQDAVSGAAQASEEAV 779
70		790 800 810 820 830 840        56

#### ATTECET OFFICE









Pecanex gene was originally discovered in *Drosophila*, encoding a large, membrane-spanning protein. The mouse homolog was recently reported. In the absence of maternal expression of the pecanex gene, the embryo develops severe hyperneuralization similar to that characteristic of Notch mutant embryos. Early gastrula embryos, lacking both maternally and zygotically expressed activity of the neurogenic pecanex locus, are shown to contain a greater than wild-type number of stably determined neural precursor cells which can differentiate into neurons in culture. Therefore it is anticipated that this novel human pecanex will be involved in neuronal differentiation, maintenance of neuronal precursors and neurological diseases.

The disclosed NOV3 nucleic acid of the invention encoding a Human homolog of the Drosophila pecanex protein includes the nucleic acid whose sequence is provided in Table 3A or a fragment thereof. The invention also includes a mutant or variant nucleic acid any of whose bases may be changed from the corresponding base shown in Table 3A while still encoding a protein that maintains its Human homolog of the Drosophila pecanex activities and physiological functions, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including nucleic acid fragments that are complementary to any of the nucleic acids just described. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way

gi 13653970 ref XP_ 009546.3  (XM_009546)	serine/threo nine kinase 15 (Homo sapiens)	403	369/403 (91%)	381/403 (93%)	0.0
gi 4507275 ref NP_0 03591.1  (NM_003600)	serine/threo nine kinase 15; Serine/threo nine protein kinase 15 (Homo sapiens)	403	369/403 (91%)	380/403 (93%)	0.0
gi 7446411 pir  JC5 974	aurora- related kinase 1 (EC 2.7) - human	403	367/403 (91%)	379/403 (93%)	0.0
gi 4507279 ref NP_0 03149.1  (NM_003158)	serine/threo nine kinase 6; Serine/threo nine protein kinase-6; serine/threo nine kinase 6 (aurora/IPL1 -like) (Homo sapiens)	402	342/403 (84%)	360/403 (88%)	0.0

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 4D.

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5
                                       Table 4D. ClustalW Analysis of NOV4
       1) NOV4 (SEQ ID NO:14)
           gi|12654873|gb|AAH01280.1|AAH01280 (BC001280) serine/threonine kinase 15 (Homo
       sapiens) (SEQ ID NO:47)
       3) gi|13653970|ref|XP_009546.3| (XM_009546) serine/threonine kinase 15 [Homo
 10
       sapiens) (SEQ ID NO:48)
       4) gi|4507275|ref|NP_003591.1| (NM_003600) serine/threonine kinase 15;
       Serine/threonine protein kinase 15 [Homo sapiens] (SEQ ID NO:49)
       5) gi | 7446411 | pir | | JC5974 aurora-related kinase 1 (EC 2.7.-.-) - human (SEQ ID
       NO:50)
15
       6) gi|4507279|ref|NP_003149.1| (NM_003158) serine/threonine kinase 6;
       Serine/threonine protein kinase-6; serine/threonine kinase 6 (aurora/IPL1-like)
       (Homo sapiens) (SEQ ID NO:51)
20
                                             20
                                                        30
                                                                    40
                                                                               50
       NOV4
                       MDOSEENCISGPVEAKTPVGGPENVLVTQQFPCQNPLPANSGQA
                       MDRSKENCISGPVKATAPVGGPKRVLVTQQFPCQNPLPVNSGQAQRVLCP
       gi | 12654873 |
                       MDRSKENCISGPVKATAPVGGPKRVLVTQQFPCQNPLPVNSGQAQRVLCP
MDRSKENCISGPVKATAPVGGPKRVLVTQQFPCQNPLPVNSGQAQRVLCP
MDRSKENCISGPVKATAPVGGPKRVLVTQQFPCQNPLPVNSGQAQRVLCP
       gi | 13653970 |
25
       gi 45072751
       gi|7446411|
                       MDRSKENCISGPVKATAPVGGPKRVLVTQQFPCQNPLPVNSGOAQRVLCP
       gi|4507279|
                                 60
                                                                             100
30
                       SNSSQRVPLQAQKLVSSHKPVQNQKQKQLQATSVPHPASRPLNNTCNSK
       NOV4
       gi|12654873|
                       SNSSORVPLQAQKLVSSHKPVQNQKQKQLQATSVPHPVSRPLNNTQKSKQ
       gi|13653970|
                       SNSSQFar{f u}PLQAQKLVSSHKPVQNQKQKQLQATSVPHPVSRPLNNTQKSKÇ
       gi | 4507275 |
                       SNSSQRVPLQAQKLVSSHKPVQNQKQKQLQATSVPHPVSRPLNNTQKSKQ
35
                       SNSSQF<mark>I</mark>PLOAOKLVSSHKPVONOKOKOLO<mark>O</mark>TSVPHPVSRPLNNTOKSKO
       gi|7446411|
```

	gi 4507279	SNSSQRVPLOAQKLVSSHKPVQNQKQKQLQATSVPHPVSRPLNNTQKSKÇ
5	NOV4 gi 12654873  gi 13653970  gi 4507275  gi 7446411  gi 4507279	110 120 130 140 150
15	NOV4 gi 12654873  gi 13653970  gi 4507275  gi 7446411  gi 4507279	160 170 180 190 200
25	NOV4 gi   12654873   gi   13653970   gi   4507275   gi   7446411   gi   4507279	210 220 230 240 250  HDATRVYLILEYTPLETVNTELQKLSKFDEQRTATYITELASALSYCHSK HDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITELANALSYCHSK HDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITELANALSYCHSK HDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITELANALSYCHSK HDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITELANALSYCHSK HDATRVYLILEYAPLGTVYRELOKLSKFDEQRTATYITELANALSYCHSK
30		260 270 280 290 300
35	NOV4 gi 12654873  gi 13653970  gi 4507275  gi 7446411  gi 4507279	TVIHRDIKPENLLLGSAGELEIAN FGWSEHAPSSRRTTLCGTLDYLPPEM RVIHRDIKPENLLLGSAGELKIAD FGWSVHAPSSRRTTLCGTLDYLPPEM RVIHRDIKPENLLLGSAGELKIAD FGWSVHAPSSRRTTLCGTLDYLPPEM RVIHRDIKPENLLLGSAGELKIAD FGWSVHAPSSRRTTLCGTLDYLPPEM RVIHRDIKPENLLLGSAGELKIAD FGWSVHAPSSRRTTLCGTLDYLPPEM RVIHRDIKPENLLLGSAGELKIAD FGWSVHAPSSRRTTLCGTLDYLPPEM
40	NOV4	310 320 330 340 350       IEGRMHDEKVDLWSLGVLCCEFLVGKPPFEANTYQETYKRISRVEFTFPD
45	gi   12654873   gi   13653970   gi   4507275   gi   7446411   gi   4507279	IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPD IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPD IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPD IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPD IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPD
50	NOV4 gi 12654873  gi 13653970	360 370 380 390 400  FVTEGARDLISRLIKHVPSQRPMLREVLEYPWITANSSKPSNCQNKESTS FVTEGARDLISRLIKHNPSQRPMLREVLEHPWITANSSKPSNCQNKESAS FVTEGARDLISRLIKHNPSQRPMLREVLEHPWITANSSKPSNCQNKESAS
55	gi 4507275  gi 7446411  gi 4507279	FVTEGARDLISRLLKHNPSQRPMLREVLEHPWITANSSKPSNCQNKESAS FVTEGARDLISRLLKHNPSQRPMLREVLEHPWITANSSKPSNCQNKESAS FVTEGARDLISRLLKHNPSQRPMLREVLEHPWITANSSKPSNCQNKESAS
60	NOV4 gi 12654873  gi 13653970  gi 4507275  gi 7446411  gi 4507279	KMS KQS KQS KQS KQS

#### Table 5B. NOV5 protein sequence (SEQ ID NO:16)

MGQSQGDGHGPRRGKKDEKDKKNKYEPLVPTRVAEKEEKTKGQDVASKLPLVTLHTQCRLKLLKLERIKDYLLM VEEFIRNQEQIKLLEEKQEEGRSKVDDLRGTPMSVGNLEEIIDDNHAIVSTSVGSEHYDSIISFVEKDLLEPGC SILLRHKVHAVIGVLMDDTGGLUVTMMKVEKAPQETYVNTGGLDNQIQEIKESMELPLPHPEYYEEMGTKPPKGV ILCGPPGTGKTLLAKAVANQTSATFLRVVGSELIQKYLGDGPKLVRQVFQVAEEHAPSIMFTDEIEAIGTKRYD SNSGGEREIQQTMLELELNQLGGFDSREDVKVIMATKQVETLDPVLIRPGRIDKKIEFHLPDEKTKKHIFQIH TSRMTLANDVTLDDLIMAKDDFSGADIKAICTEAGLMALREHRMKATNEDFKKSIESVLYKKHEGIPEGLYL

The full amino acid sequence of the protein of the invention was found to have 383 of 442 amino acid residues (86%) identical to, and 405 of 442 amino acid residues (91%) similar to, the 440 amino acid residue ptnr:SWISSPROT-ACC:P49014 protein from *Mus musculus* (Mouse), and *Rattus norvegicus* (Rat) (26S Protease Regulatory Subunit 4 (P26S4) (E = 1.7e<sup>-200</sup>).

NOV5 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 5C.

Table 5C. BLAST results for NOV5							
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect		
gi 4506207 ref NP_0 02793.1  (NM_002802)	proteasome (prosome, macropain) 26S subunit, ATPase, 1; Proteasome 26S subunit, ATPase, 1 [Homo sapiens]	440	382/442 (86%)	405/442 (91%)	0.0		
gi 6679501 ref NP_0 32973.1  (NM_008947)	protease (prosome, macropain) 26S subunit, ATPase 1 [Mus musculus]	440	383/442 (86%)	405/442 (90%)	0.0		
gi 345717 pix  A444  68	26S proteasome regulatory chain 4 (validated) - human	440	381/442 (86%)	404/442	0.0		
gi 16741033 gb AAH1 6368.1 AAH16368 (BC016368)	protease (prosome, macropain) 26S subunit, ATPase 1 [Homo sapiens]	440	382/442 (86%)	404/442 (90%)	0.0		
gi 2492516 8p Q9073 2 PRS4_CHICK	26S PROTEASE REGULATORY SUBUNIT 4 (P26S4)	440	378/442 (85%)	402/442 (90%)	0.0		

10

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 5D.

#### Table 5D ClustalW Analysis of NOV5

<sup>1)</sup> NOV5 (SEQ ID NO:16)
2) gi|4506207|ref|NP\_002793.1| (NM\_002802) proteasome (prosome, macropain) 26S subunit, ATPase, 1; Proteasome 26S subunit, ATPase, 1 [Homo sapiens] (SEQ ID NO:52)
3) gi|6679501|ref|NP\_032973.1| (NM\_008947) protease (prosome, macropain) 26S subunit, ATPase 1 [Mus musculus] (SEQ ID NO:53)
4) gi|345717|pir||A44468 26S proteasome regulatory chain 4 [validated] - human (SEQ ID NO:54)

5	subunit, ATPa	033 gb AAH16368.1 AAH16368 (BC016368) protease (prosome, macropain) 2 use 1 (Homo sapiens) (SEQ ID NO:55) .6 sp Q90732 PRS4_CHICK 26S PROTEASE REGULATORY SUBUNIT 4 (P26S4) (SE	
		10 20 30 40 50	
10	NOVS gi 4506207  gi 6679501  gi 345717  gi 16741033  gi 2492516	MGQSOGDGHGPRRGKKDEKDKKNKYEPLVPTRVASKESKTKGGDVASKLP MGQSQSGGHGPGGKKDDEDKKKKYEPPVPTRVASKEKKKTKGDDVASKLP MGQSQSGGHGPGGGKKDDEDKKKKYEPPVPTRVGKKKKKTKGPDAASKLP MGQSQSGGHGPGGGKKDDEDKKKKYEPPVPTRVGKKKKKREPDAASKLP MGQSQSGGHGPGGGKKDDEDKKKKYEPPVPTRVGKKKKKREPDAASKLP MGQSQSGGHGPGGGKKDDKDKKKKYEPPVPTRVGKKKKKTKGPDAASKLP MGQSQSGGHGPGGGKKDDKDKKKKYEPPVPTRVGKKKKKTKGPDAASKLP	
15		60 70 80 90 100	
20	NOV5 gi 4506207  gi 6679501  gi 345717  gi 16741033  gi 2492516	LVTPHTQCRLKLLKLERIKDYLLMVEEFIRNQEQIKLLEEKQEEGRSKVD LVTPHTQCRLKLLKLERIKDYLLMEEEFIRNQEQMKPLEEKQEERSKVD LVTPHTQCRLKLLKLERIKDYLLMEEEFIRNQEQMKPLEEKQEEERSKVD LVTPHTQCRLKLLKLERIKDYLLMEEEFIRNQEQMKPLEEKQEEERSKVD LVTPHTQCRLKLLKLERIKDYLLMEEEFIRNQEQMKPLEEKQEEERSKVD LVTPHTQCRLKLLKLERIKDYLLMEEEFIRNQEQMKPLEEKQEEERSKVD LVTPHTQCRLKLLKLERIKDYLLMEEEFIRNQEQMKPLEEKQEEERSKVD	
25		110 120 130 140 150	
30	NOV5 gi 4506207  gi 6679501  gi 345717  gi 16741033  gi 2492516	DLRGTPMSVCNLEEIIDDNHAIVSTSVGSEHYDSIISFVEKDLLEPGCSI DLRGTPMSVGTLEEIIDDNHAIVSTSVGSEHYVSILSFVDKDLLEPGCSV DLRGTPMSVGTLEEIIDDNHAIVSTSVGSEHYVSILSFVDKDLLEPGCSV DLRGTPMSVGTLEEIIDDNHAIVSTSVGSEHYVSILSFVDKDLLEPGCSV DLRGTPMSVGTLEEIIDDNHAIVSTSVGSEHYVSILSFVDKDLLEPGCSV DLRGTPMSVGTLEEIIDDNHAIVSTSVGSEHYVSILSFVDKDLLEPGCSV	
		160 170 180 190 200	
35 40	NOV5 gi 4506207  gi 6679501  gi 345717  gi 16741033  gi 2492516	LLRHKVHAVIGVLMDDTGPLVTMKVEKAPQETYVNTGGLDNQIQEIKES LLNHKVHAVIGVLMDDTDPLVTVMKVEKAPQETYADIGGLDNQIQEIKES LLNHKVHAVIGVLMDDTDPLVTVMKVEKAPQETYADIGGLDNQIQEIKES LLNHKVHAVIGVLMDDTDPLVTVMKVEKAPQETYADIGGLDNQIQEIKES LLNHKVHAVIGVLMDDTDPLVTVMKVEKAPQETYADIGGLDNQIQEIKES LLNHKVHAVIGVLMDDTDPLVTVMKVEKAPQETYADIGGLDNQIQEIKES LLNHKVHAVIGVLMDDTDPLVTVMKVEKAPQETYADIGGLDNQIQEIKES	
		210 220 230 240 250	
45	NOV5 gi 4506207  gi 6679501  gi 345717  gi 16741033  gi 2492516	MELPLPHPEY YEEMGIKPPKGVILGGPPGTGKTLLAKAVANQTSATFLRV VELPLTHPEY YEEMGIKPPKGVILGGPPGTGKTLLAKAVANQTSATFLRV VELPLTHPEY YEEMGIKPPKGVILYGPPGTGKTLLAKAVANQTSATFLRV VELPLTHPEY YEEMGIKPPKGVILYGPPGTGKTLLAKAVANQTSATFLRV VELPLTHPEY YEEMGIKPPKGVILYGPPGTGKTLLAKAVANQTSATFLRV VELPLTHPEY YEEMGIKPPKGVILYGPPGTGKTLLAKAVANQTSATFLRV VELPLTHPEY YEEMGIKPPKGVILYGPPGTGKTLLAKAVANOTSATFLRV	
50		260 270 280 290 300	
55	NOV5 gi 4506207  gi 6679501  gi 345717  gi 16741033  gi 2492516	VGSELIQKYLGDGPKLVROVFOVAEEHAPSIMFIDEIDAIGTKRYDSNSG VGSELIQKYLGDGPKLVRELFRVAEEHAPSIVFIDEIDAIGTKRYDSNSG VGSELIQKYLGDGPKLVRELFRVAEEHAPSIVFIDEIDAIGTKRYDSNSG VGSELIQKYLGDGPKLVRELFRVAEEHAPSIVFIDEIDAIGTKRYDSNSG VGSELIQKYLGDGPKLVRELFRVAEEHAPSIVFIDEIDAIGTKRYDSNSG VGSELIQKYLGDGPKLVRELFRVAEEHAPSIVFIDEIDAIGTKRYDSNSG	
60		310 320 330 340 350	
65	NOV5 gi 4506207  gi 6679501  gi 345717  gi 16741033  gi 2492516	GEREIQTMLELELLNOLGGFDSREDVKVIMATKOVETLDFVLIRPGRID GEREIQRTM LELLNQLDGFDSRGDVKVIMATNRIETLDFALIRPGRID GEREIQRTM LELLNQLDGFDSRGDVKVIMATNRIETLDFALIRPGRID GEREIQRTM LELLNQLDGFDSRGDVKVIMATNRIETLDFALIRPGRID GEREIQRTM LELLNQLDGFDSRGDVKVIMATNRIETLDFALIRPGRID GEREIQRTM LELLNQLDGFDSRGDVKVIMATNRIETLDFALIRPGRID GEREIQRTM LELLNQLDGFDSRGDVKVIMATNRIETLDFALIRPGRID	
70		360 370 380 390 400        72	

```
kiefhlpdektkk<mark>h</mark>ifqihtsrmtla<mark>n</mark>dvtlddlimakdd<mark>e</mark>sgadikai
Rkiefplpdektkkrifqihtsrmtladdvtlddlimakddlsgadikai
       NOVS
       gi|4506207|
       gi|6679501|
                          RKIEFPLPDEKTKKRIFQIHTSRMTLADDVTLDDLIMAKDDLSGADIKAI
                          RKIEFPLPDEKTKKRIFQIHTSRMTLADDVTLDDLIMAKDDLSGADIKAI
       gi|345717|
                          RKIEFPLPDEKTKKRIFQIHTSRMTLADDVTLDDLIMAKDDLSGADIKAI
       gi|16741033|
                          RKIEFPLPDEKTKKRIFQIHTSRMTLADDVTLD<mark>E</mark>LIMAKDDLSGADIKAI
       gi | 2492516 |
                                                               430
                          CTEAGLMALREHRMKATNEDFKKSIEŠVLYKKHEGIPEGLYL
CTEAGLMALRERRMKVTNEDFKKSKENVLYKKQEGTPEGLYL
10
       NOV5
       gi|4506207|
       gi|6679501
                          CTEAGLMALRERRMKVTNEDFKKSKENVLYKKQEGTPEGLYL
       gi|345717|
                          CTEAGLMALRERRMKVTNEDFKKSKENVLYKKQEGTPEGLYL
       gi|16741033|
                          CTEAGLMALRERRMKVTNEDFKKSKENVLYKKQEGTPEGLYL
15
                          CTEAGLMALRERRMKVTNEDFKKSKEN<mark>F</mark>LYKK<mark>T</mark>EGTPEGLYL
       gi | 2492516 |
```

20

Tables 5E-F list the domain description from DOMAIN analysis results against NOV5.

This indicates that the NOV5 sequence has properties similar to those of other proteins known to contain this domain.

#### Table 5E. Domain Analysis of NOV5

gnl | Pfam | pfam00004, AAA, ATPase family associated with various
cellular activities (AAA). AAA family proteins often perform
chaperone-like functions that assist in the assembly, operation, or
disassembly of protein complexes (SEQ ID NO:101)
CD-Length = 186 residues, 100.0% aligned
Score = 190 bits (483), Expect = 1e-49

```
NOV 4: 221 GVILCGPPGTGKTLLAKAVANQTSATFLRVVGSELIQKYLGDGPKLVRQVFQVAEEHAPS 280
                - |+ + ||||+ ||+|+ ||||| +| +| + ||
25
                GILLYGPPGTGKTLLAKAVAKELGVPFIEISGSELLSKYVGESEKLVRALFSLARKSAPC
     Sbjct: 1
     NOV 4: 281
                IMFTDEIEAIGTKRYDSNSGGEREIQQTMLELELLNQLGGFDSREDVKVIMATKQVETLD 340
                Sbjct:
30
     NOV 4: 341
                PVLIRPGRIDKKIEFHLPDEKTKKHIFQIHTSRMTLANDVTLDDLIMAKDDFSGADIKAI
                                                                      400
                | |+|||| |++|| ||||+ + |||+|| + || ||||++
                PALLRPGRFDRRIEVPLPDEEERLEILKIHLKKKPLEKDVDLDEIARRTPGFSGADLAAL
     Sbjct: 117
35
     NOV 4: 401
                CTEAGLMALR 410
                  | | | | | | | | |
     Sbjct: 177
                CREAALRAIR 186
```

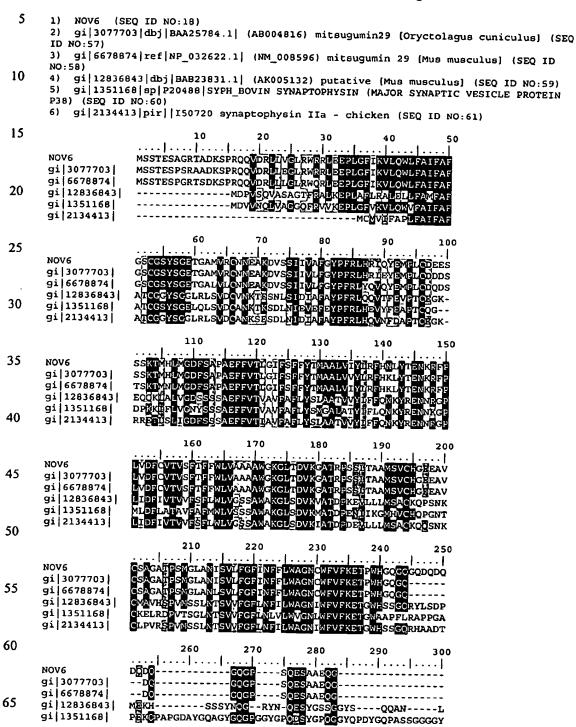
#### Table 5F. Domain Analysis of NOV5

gnl | Smart | smart 00382, AAA, ATPases associated with a variety of
cellular activities; AAA. This profile/alignment only detects a
fraction of this vast family. The poorly conserved N-terminal helix is
missing from the alignment. (SEQ ID NO:102)
CD-Length = 151 residues, 100.0% aligned
Score = 61.6 bits (148), Expect = 9e-11

```
40 NOV 4: 218 PPKGVILCGPPGTGKTLLAKAVANQTSATFLRVV-------GSELIQK 258
| + |+ |+ |||+|| | |+ |+ |
Sbjct: 1 PGEVVLIVGPPGSGKTTLARALARELGPDGGGVIYIDGEDLREEALLQLLRLLVLVGEDK 60
```

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 6D.

## Table 6D Clustal W Sequence Alignment



15

Table 6E lists the domain description from DOMAIN analysis results against NOV6.

This indicates that the NOV6 sequence has properties similar to those of other proteins known to contain this domain.

```
Table 6E. Domain Analysis of NOV6

gnl | Pfam | pfam 01284 | Synaptophysin | Synaptophysin | synaptoporin. (SEQ ID NO:103)

CD-Length = 298 residues, 70.8% aligned

Score = 244 bits (622), Expect = 6e-66
```

```
NOV 5: 29
                RRLEEPLGFIKVLQWLFAIFAFGSCGSYSGETGAMVRCNNEAKDVSSIIVAFGYPFRLHR
                    1 [ ]+ + + + + | + | | | | | | | | |
20
                MVIFAPLGFVKVLQWVFAIFAFATCGGYSGELQLSVDCANKTESDLNIDIAFAYPFRLHE
     Sbict: 3
     NOV 5:
                IQYEMPLCDEESSSKTMHLMGDFSAPAEFFVTLGIFSFFYTMAALVIYLRFHNLYTENKR
                          Sbjct: 63
                VTFEAPTC-EGDEKKNIALVGDSSSAEFFVTVAVFAFLYSLAALATYIFFONKYRENNK
25
                FPLVDFCVTVSFTFFWLVAAAAWGKGLTDVKGATRPSSLTAAMSVCHGEEAVCSAGATPS
     NOV 5:
            149
                                                                     208
                 1 11
     Sbjct:
            122
                GPLIDFIATAVFAFLWLVGSSAWAKGLSDVKMATDPEEIIKGMHACHQPGNKCKELHDPV
30
     NOV 5:
            209
                MGLANISVLFGFINFFLWAGNCWFVFKETPWH
                   1 11+111+11 11111 1111111
     Sbict:
                MSGLNTSVVFGFLNFILWAGNIWFVFKETGWA
```

In skeletal muscle, excitation-contraction (E-C) coupling requires the conversion of the

depolarization signal of the invaginated surface membrane, namely the transverse (T-) tubule,
to Ca2+ release from the sarcoplasmic reticulum (SR) (Takeshima H et al., Biochem J 1998
Apr 1;331 ( Pt 1):317-22 / PMID: 9512495, UI: 98180964). Signal transduction occurs at the
junctional complex between the T-tubule and SR, designated as the triad junction, which
contains two components essential for E-C coupling, namely the dihydropyridine receptor as
the T-tubular voltage sensor and the ryanodine receptor as the SR Ca2+-release channel.
However, functional expression of the two receptors seemed to constitute neither the signaltransduction system nor the junction between the surface and intracellular membranes in
cultured cells, suggesting that some as-yet-unidentified molecules participate in both the
machinery. In addition, the molecular basis of the formation of the triad junction is totally

## Table 7B. Encoded NOV7 protein sequence (SEQ ID NO:20).

LTGREVLTPFPGLGTAAAPAQGGAHLKQCDLLKLSRRQKQLCRREPGLAETLRDAAHLGLLECQFQFRHERWNCS LEGRMGLLKRGFKETAFLYAVSSAALTHTLARACSAGRMERCTCDDSPGLESRQAWQWGVCGDNLKYSTKFLSNF LGSKRGNKDLRARADAHNTHVGIKAVKSGLRTTCKCHGVSGSCAVRTCWKQLSPFRETGQVLKLRYDSAVKVSSA TNEALGRLELWAPARQGSLTKGLAPRSGDLVYMEDSPSFCRPSKYSPGTAGRVCSREASCSSLCCGRGYDTQSRL VAFSCHCQVQWCCYVECQQCVQEELVYTCKH

The disclosed NOV7 amino acid sequence has 205 of 330 amino acid residues (62%) identical to, and 252 of 330 amino acid residues (76%) similar to, the 354 amino acid residue ptnr:SWISSPROT-ACC:O42280 protein from *Gallus gallus* (Chicken) (WNT-14 Protein Precursor) (E = 1.3e<sup>-114</sup>).

The tissue expression of NOV7 is predicted to be expressed in brain because of the expression pattern of (GENBANK-ID: gb:GENBANK-ID:AF031168|acc:AF031168.1) a closely related *Gallus gallus* Wnt-14 protein (Wnt-14) mRNA, complete cds homolog.

NOV7 also has homology to the amino acid sequences shown in the BLASTP data listed in Table 7C.

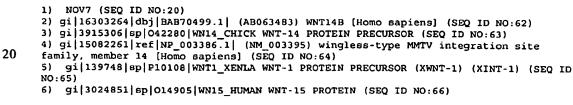
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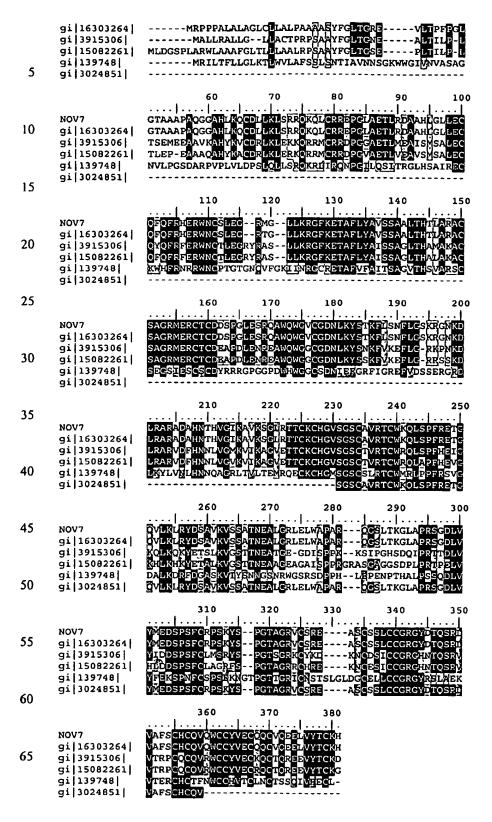
Table 7C. BLAST results for NOV7							
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect		
gi 16303264 dbj BAB 70499.1  (AB063483)	WNT14B [Homo sapiens]	357	330/331 (99%)	330/331 (99%)	e-175		
gi 3915306 sp 04228 0 WN14_CHICK	WNT-14 PROTEIN PRECURSOR	354	204/332 (61%)	253/332 (75%)	e-109		
gi 15082261 ref NP_ 003386.1  (NM_003395)	wingless-type MMTV integration site family, member 14 [Homo sapiens]	365	209/335 (62%)	255/335 (75%)	e-108		
gi 139748 sp P10108  WNT1_XENLA	WNT-1 PROTEIN PRECURSOR (XWNT- 1) (XINT-1)	371	120/313 (38%)	175/313 (55%)	5e-58		
gi 3024851 sp 01490 5 WN15_HUMAN	WNT-15 PROTEIN	120	120/120 (100%)	120/120 (100%)	2e-56		

The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 7D.

#### Table 7D Information for the ClustalW proteins







VEAVSMSALECOFOFRFERWNCTLEGRYRASLLKRGFKETAFLYAISSAGLTHALAKACSAGRMERCTCDE APDLENREGWKWGGCSEDIEFGGMVSREFADARENRPDARSAMNRHNNEAGRQVIKAGVETTCKCHGVSGS CTVRTCWRQLAPFHEVGKHLKHKYESALKVGSTTNEAAGEAGAISPPRGRASGAGGSDPLPRTPELVHLDD SPSFCLAGRFSPGTAGRRCHREKNCESICCGRGHNTOSRVVTRPCQCQVRWCCYVECRQCTQREEVYTCKG

The disclosed NOV8 amino acid sequence has 270 of 354 amino acid residues (76%) identical to, and 310 of 354 amino acid residues (87%) similar to, the 354 amino acid residue ptnr:SWISSPROT-ACC:O42280 protein from *Gallus gallus* (Chicken) (WNT-14 Protein Precursor (1.2e<sup>-151</sup>).

NOV8 is expressed in at least brain. This information was derived by determining the tissue sources of the sequences that were included in the invention including but not limited to SeqCalling sources, Public EST sources, Literature sources, and/or RACE sources.

In addition, the sequence is predicted to be expressed in brain because of the expression pattern of (GENBANK-ID: gb:GENBANK-ID:AF031168|acc:AF031168.1) a closely related [Gallus gallus Wnt-14 protein (Wnt-14) mRNA, complete cds].

NOV8 also has homology to the amino acid sequence shown in the BLASTP data listed in Table 8C.

Table 8C. BLAST results for NOV8						
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect	
gi 15082261 ref NP_0 03386.1  (NM_003395)	wingless-type MMTV integration site family, member 14 [Homo sapiens]	365	306/340 (90%)	321/340 (94%)	e-167	
gi 3915306 sp 042280  WN14 CHICK	WNT-14 PROTEIN PRECURSOR	354	270/357 (75%)	310/357 (86%)	e-142	
gi 16303264 dbj BAB7 0499.1  (AB063483)	WNT14B [Homo sapiens]	357	193/339 (56%)	244/339 (71%)	e-100	
gi 7105447 ref NP_03 3548.1  (NM_009522)	wingless-related MMTV integration site 3A [Mus musculus]	352	141/311 (45%)	179/311 (57%)	2e-62	
gi 5821261 dbj BAA83 743.1  (AB024080)	Wnt-3a (Gallus gallus)	376	139/311 (44%)	179/311 (56%)	3e-62	

15

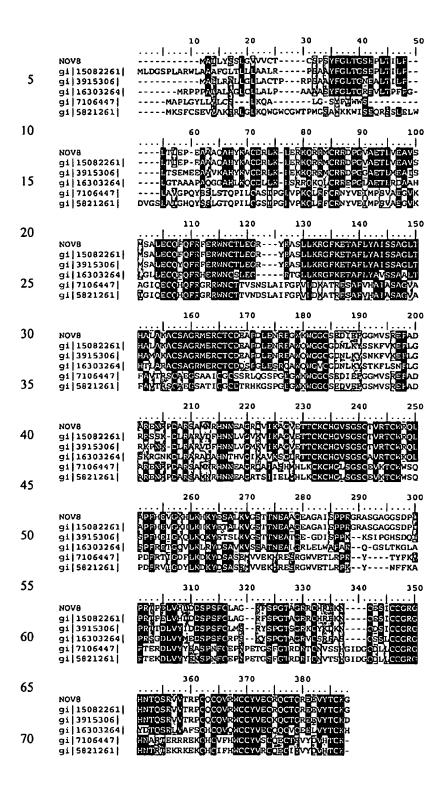
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The homology of these sequences is shown graphically in the ClustalW analysis shown in Table 8D.

#### Table 8D. Information for the ClustalW proteins

1) NOV8 (SEQ ID NO:22)
20 gi|15082261|ref|NP\_003386.1| (NM\_003395) wingless-type MMTV integration site family, member 14 [Homo sapiens] (SEQ ID NO:64)
3) gi|3915306|sp|042280|WN14\_CHICK WNT-14 PROTEIN PRECURSOR (SEQ ID NO:63)
4) gi|16303264|dbj|BaP70499.1| (AB063483) WNT14B [Homo sapiens] (SEQ ID NO:62)
5) gi|7106447|ref|NP\_033548.1| (NM\_009522) wingless-related MMTV integration site
3A [Mus musculus] (SEQ ID NO:67)
6) gi|5821261|dbj|BAA83743.1| (AB024080) Wnt-3a [Gallus gallus] (SEQ ID NO:68)



The disclosed NOV9 polypeptide has homology to the amino acid sequences shown in the BLASTP data listed in Table 9C.

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
ptnr:pir-id:A53791	beta-adrenergic- receptor kinase (EC 2.7.1.126) 1 - human	689	495/497 (99%)	495/497 (99%)	0.0
ptnr:SWISSPROT- ACC:P25098	Beta-adrenergic receptor kinase 1 (EC 2.7.1.126)	689	494/497 (99%)	495/497 (99%)	0.0
ptnr:SPTREMBL- ACC:Q99LL8	SIMILAR TO ADREMERGIC, BETA, RECEPTOR KINASE 1 - Mus musculus	687	490/495 (98%),	493/495 (99%)	0.0
ptnr:SWISSPROT- ACC:P26817	Beta-adrenergic receptor kinase 1	689	489/497 (98%)	493/497 (99%)	0.0
ptnr:SPTREMBL- ACC:Q99MK8	G PROTEIN RECEPTOR KINASE 2	689	490/497 (98%)	494/497 (99%)	0.0

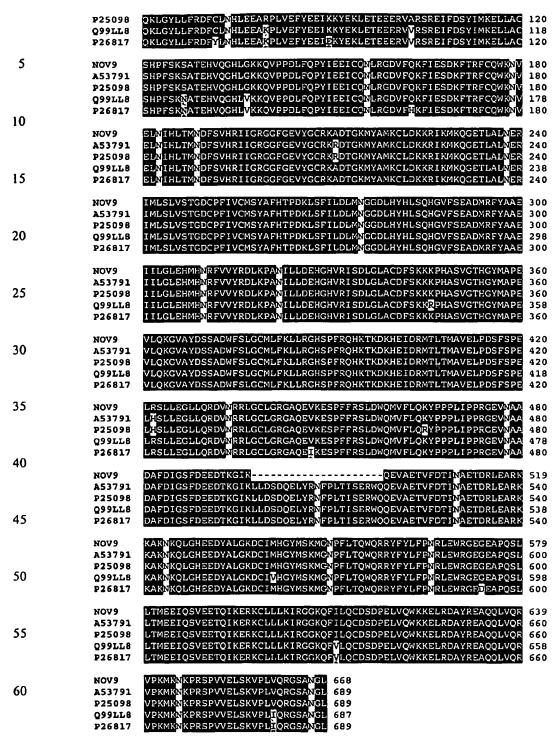
The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 9D. In the ClustalW alignment of the NOV9 proteins, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be altered to a much broader extent without altering protein structure or function.

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## Table 9D. ClustalW Analysis of NOV9

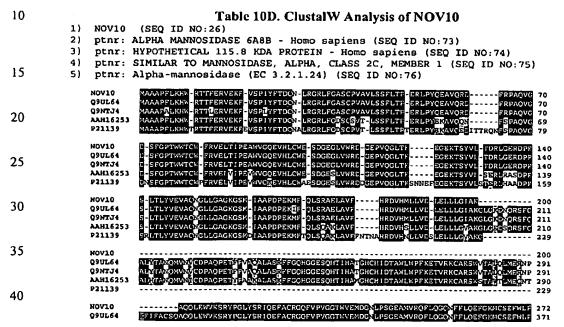
15	<ol> <li>NOV9 (SEQ ID NO:24)</li> <li>ptnr:pir-id:A53791 beta-adrenergic-receptor kinase (EC 2.7.1.126) 1 (SEQ ID NO:69)</li> </ol>
	3) ptnr:SWISSPROT-ACC:P25098 Beta-adrenergic receptor kinase 1 (EC 2.7.1.126)
20	(SEQ ID NO:70) 4) ptnr:SPTREMBL-ACC:Q99LL8 SIMILAR TO ADRENERGIC, BETA, RECEPTOR KINASE 1 - Mus musculus (Mouse) (SEO ID NO:71)
20	musculus (Mouse) (SEQ ID NO:71) 5) 6) ptnr:SWISSPROT-ACC:P26817 Beta-adrenergic receptor kinase 1 (EC 2.7.1.126) (Beta-ARK-1) (SEQ ID NO:72)
	NOV9 MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIRSVMOKYLEDRGEVTFEKIFS 60
25	A53791 MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIRSVMOKYLEDRGEVTFEKIFS 60
	P25098 MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIRSVMQKYLEDRGEVTFEKIFS 60
	Q99LL8DLEAVLADVSYLMANEKSKATPAARASKKILLPEPSIRSVMQKYLEDRGEVTFEKIFS 58
	P26817 MADLEAVLADVSYLMAMEKSKATPAARASKKILLPEPSIRSVMOKYLEDRGEVTFEKIFS 60
30	NOV9 QKLGYLLFRDFCLNHLEEARPLVEFYEEIKKYEKLETEEERVARSREIFDSYIMKELLAC 120
	A53791 OKLGYLLFRDFCLNHLEEARPLVEFYEEIKKYEKLETEEERVARSREIFDSYINKELLAC 120



Tables 9E-9L list the domain descriptions from DOMAIN analysis results against NOV9. This indicates that the NOV9 sequence has properties similar to those of other proteins known to contain this domain.

Gene Index/ Identifier		Length (aa)	Identity (%)	Positives (%)	Expect
ptnr:SPTREMBL- ACC:Q9UL64	ALPHA MANNOSIDASE 6A8B - Homo sapiens	1062	763/771 (99%)	767/771 (99%)	0.0
ptnr:SPTREMBL- ACC:Q9NIJ4	HYPOTHETICAL 115.8 KDA PROTEIN - Homo sapiens	1040	715/722 (99%)	718/722 (99%)	0.0
ptnx:TREMBLNEW- ACC:AAH16253	SIMILAR TO MANNOSIDASE, ALPHA, CLASS 2C, MEMBER 1	1039	635/730 (89%),	692/730 (94%)	0.0
ptnr:SWISSPROT- ACC:P21139	Alpha-mannosidase (EC 3.2.1.24)	1040	625/731 (85%)	661/731 (90%)	0.0
ptnr:SPTREMBL- ACC:Q13358	ALPHA-MANNOSIDASE - Homo sapiens	425	425/425 (100%)	425/425 (100%)	0.0

The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 10D. In the ClustalW alignment of the NOV10 protein, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be altered to a much broader extent without altering protein structure or function.



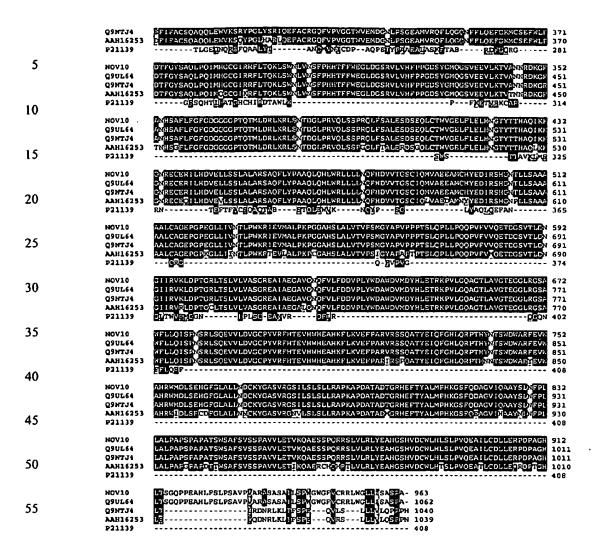
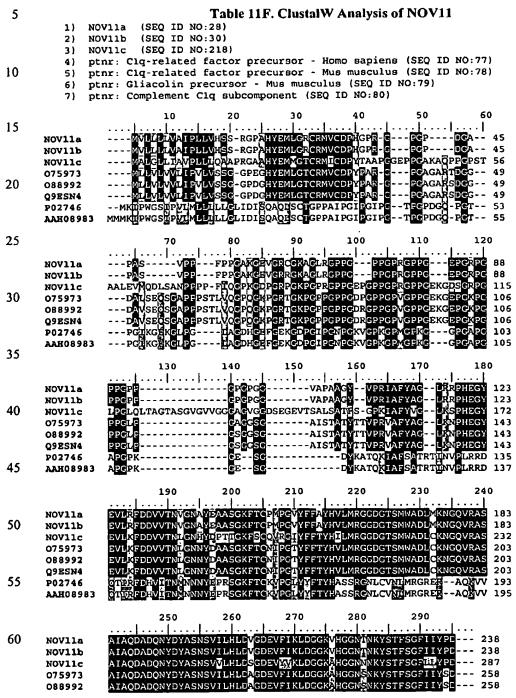


Table 10E lists the domain description from DOMAIN analysis results against NOV10. This indicates that the NOV10 sequence has properties similar to those of other proteins known to contain this domain.

Model	Description	Score	E-value
Glyco_hydro_38 (SEQ ID NO:111)	(InterPro) Glycosyl hydrolases family 38	140.5	le-39
	domain 1 of 2, from 230 to 332: score 89.2, E  *->vtGGWVMnDEAttHyedlIdQlteGHqfLeenfGsdvkF   + + + + ++++++++++ + + + +++ ++++ ++	PkvgWsIDP + ++ +	
	*->vtGGWVMnDEAttHyedlIdQlteGHqfLeenfGsdvkF  + +  +   + +++ ++++ ++  +  + ++   + 230 VGGTWVEMDGNLPSGEAMVRQFLQGQNFFLQEFGKMC	PkvgWsIDP + ++ + CSEFWLPDT 27	7 <b>4</b>
	*->vtGGWVMnDEAttHyedlIdOlteGHqfLeenfGsdvkF  + +  +   + +++ ++++ ++  +  + ++   +	PkvgWsIDP + ++ + CSEFWLPDT 27 rWRqswslt	74

functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be altered to a much broader extent without altering protein structure or function.



Q9ESN4		258
P02746	TFCDYAYNTEOVTHGGMULKLEOGENVELGATDKYGLLEMEGANSTESGELLEPDMEA TFCDYAYNTEOVTHGGMULKLEOGENVELGATDKYGLLEMEGANSTESGELLEPDMEA	251
AAH08983	TFCDYAYNTEOVTEGGYYLKLECCENVELCATDKNELLCMEGANSIFSGFEREPDMEA	253

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Tables 11E-11F list the domain descriptions from DOMAIN analysis results against NOV11. This indicates that the NOV11 sequence has properties similar to those of other proteins known to contain this domain.

#### Table 11E. Domain Analysis of NOV11

gnl|Smart|smart00110, C1Q, Complement component C1q domain.; Globular
domain found in many collagens and eponymously in complement C1q. When
part of full length proteins these domains form a 'bouquet' due to the
multimerization of heterotrimers. The C1q fold is similar to that of
tumour necrosis factor. (SEQ ID NO:104)
CD-Length = 132 residues, 99.2% aligned
Score = 113 bits (283), Expect = 1e-26

```
Query: 108
                   PRIAFYAGL--RRPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGG
                   11 11
                               11
                                     + +||| |+ |
                                                    | | + ++|||||||+||||+|+||+
15
                   PRSAFSVIRSTNRPPPPGQPVRFDKVLYNQQGHYDPSTGKFTCPVPGVYYFSYHIESK--
      Sbjct: 2
                   {\tt DGTSMWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHG-GNT}
      Query: 166
                                                                                  224
                                              1 11
                                                     +| | ||+|+++||
      Sbjct: 60
                   -GRNVKVSLMKNGIQVMRECDEYQKGLYQVASGGALLQLRQGDQVWLELDDKKNGLYAGE 118
20
                   NKYSTFSGPIIYPD
      Query: 225
                                   238
                      111111+++11
      Sbjct: 119
                   EVDSTFSGFLLFPD
```

25

40

#### Table 11F. Domain Analysis of NOV11

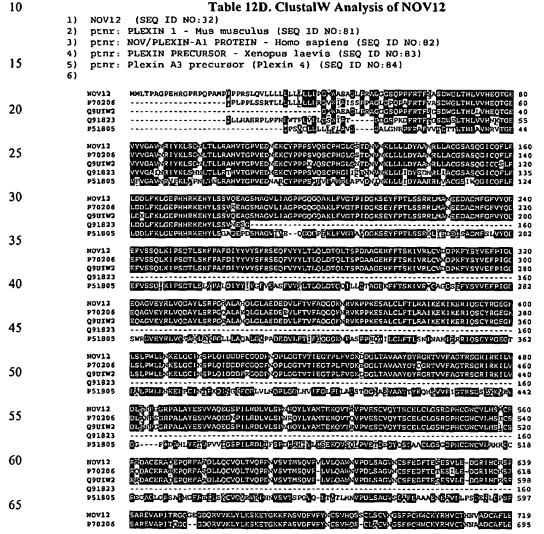
gnl|Pfam|pfam00386, Clq, Clq domain. Clq is a subunit of the Cl enzyme
complex that activates the serum complement system. (SEQ ID NO:112)
CD-Length = 125 residues, 100.0% aligned
Score = 102 bits (253), Expect = 3e-23

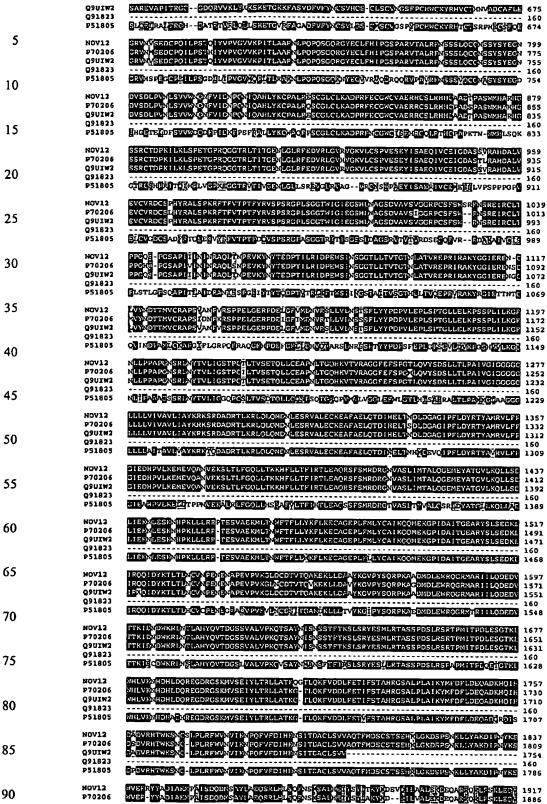
```
Query: 111
                  AFYAGLR-RPHEGYEVLRFDDVVTNVGNAYEAASGKFTCPMPGVYFFAYHVLMRGGDGTS
                               + + ||+|+ | | | + |+|||||+||+||+|| + ||+ ||+
      Sbjct: 1
                  AFTAIRSTRPPAPGQPVIFDEVLYNQQGHYDPATGKFTCPVPGLYYFNFHVSSK---GTN
30
      Query: 170
                  MWADLMKNGQVRASAIAQDADQNYDYASNSVILHLDVGDEVFIKLDGGKVHG--GNTNKY
                                 + | | | + | | | |+++| + + |
      Sbict: 58
                  VCVSLMRNGVPVMSFCDEYAKGTYQVASGGAVLQLRQGDRVWLELDDKQTNGLLGGEGVH 117
35
      Query:
             228
                  STFSGFII
                  | ||||++
      Sbjct: 118
                  SVFSGFLL
                           125
```

The first component of complement system is a calcium-dependent complex of the 3 subcomponents Clq, Clr, and Cls. Subcomponent Clq binds to immunoglobulin complexes

ptnr:SPTREMBL- ACC:P70208	PLEXIN 3 - Mus musculus	1872	1245/1874 (66%)	1478/1874 (78%)	0.0

The homology between these and other sequences is shown graphically in the ClustalW analysis shown in Table 12D. In the ClustalW alignment of the NOV12 protein, as well as all other ClustalW analyses herein, the black outlined amino acid residues indicate regions of conserved sequence (i.e., regions that may be required to preserve structural or functional properties), whereas non-highlighted amino acid residues are less conserved and can potentially be altered to a much broader extent without altering protein structure or function.





```
| 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1754 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 | 1755 |
```

Tables 12E-12N list the domain descriptions from DOMAIN analysis results against NOV12. This indicates that the NOV12 sequence has properties similar to those of other proteins known to contain this domain.

```
Table 12E. Domain Analysis of NOV12

gnl|Smart|smart00630, Sema, semaphorin domain (SEQ ID NO:113)

CD-Length = 430 residues, 100.0% aligned

Score = 242 bits (618), Expect = 1e-64
```

15 LTHLVVHEQTGEVYVGAVNRIYKLSGNLTLLRAHVTGPVEDNEKCYPPPSVQSCPHGLGS 128 Query: 69 | +|++ | | +||| ||+| || || || + | | || LQNLLLDEDNGTLYVGARNRLYVLSLNLISEAEVKTGPVLSSPDCEEC--VSKGKDPP--Sbjct: 1 20 TDNVNK-LLLLDYAANRLLACGS-ASQGICQFLRLDDLFKLGEPHHRKEHYLSSVQEAGS 186 Query: 129 Sbjct: 57 MAGVLIAGPPGQGQAKLFVGTPID--GKSEYFPTLSSRRLMANEEDADMFGFVYODEFVS Query: 187 25 11+1 +1+111 1 1 STAVLVDG------PSLRTVL Sbjct: 116 Query: 245 SQLKIPSDTLSKFPAFDIYYVYSFRSEQFVYYLTLQLDTQLTSPDAAGEHFFTSKIVRLC 304 + + + + ||+| | ||+ + | |++ |+|
YDSRWLN-----EPNFVYAFESGDFVYF----FFRETAVEDENCGKAVVSRVARVC 30 Sbjct: 162 Ouerv: 305 VDD------PKFYSYVEFPIGC---EQAGVEYRLVQDAYLSRPGRALAHQLGLAEDED |+|+++ +| + + +| |+| | KNDVGGPRSLSKKWTSFLKARLECSVPGEFPFYFNELQAAFLLPAG-----SESDD Sbjct: 209 35 Query: 354 VLFTVFAQGQKNRVKPPKESALCLFTLRAIKEKIKERIQSCYRGEGKLSL----PWLLNK 409 1 11+1 1+1 1 + 1 + 1 + VLYGVPSTS----SNPIPGSAVCAFSLSDINAVFNEPFKECETGNSQWLPYPRGLVPFPR 315 Sbjct: 260 40 Query: 410 ELGCINSPLQI----DDDFC-GQDFNQPLGGTVTIEGTPLFV--DKDDGLTAVAA----Y 458 | |+|| || + + |||| | + ||++|
PGTCPNTPLSSKDLPDDVLNFIKTHPLMDEVVQPLTGRPLFVKTDSNYLLTSIAVDRVRT 375 Sbjct: 316 DYRGRTVVFAGTRSGRIRKILVDLSNPGGRPALAYESVVAQEGSPILRDLVLSPNH 514 Query: 459 45 ||+| || || |+++ |+ + | | | ||+ ||||| DGGNYTVLFLGTSDGRILKVVLSRSSSSSESVVLEEISVFDPGSPV-SDLVLSPKK 430 Sbjct: 376

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